File

L2 ANSWER 1 OF 1 MEDLINE
AN 91209917 MEDLINE
DN 91209917
TI Glucosyltransferase gene polymorphism among Streptococcus mutans strains.
AU Chia J S; Hsu T Y; Teng L J; Chen J Y; Hahn L J; Yang C S
CS School of Dentistry, National Taiwan University, Taipei, Republic of China..
SO INFECTION AND IMMUNITY, (1991 May) 59 (5) 1656-60.
Journal code: GO7. ISSN: 0019-9567.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199108
AB Genetic polymorphisms in genes coding for the glucosyltransferases were detected among Streptococcus mutans serotype c strains by Southern blot analysis with DNA probes located within the **gtfB gene** (H. Aoki, T. **Shiroza**, M. Hayakawa, S. Sato, and H. K. Kuramitsu, Infect. Immun. 53:587-594, 1986). Restriction endonucleases were used to examine genomic DNAs isolated from serotype a to h strains. The variations were readily detected among 33 strains of serotype c by EcoRI and PstI restriction enzyme digestions. Serotypes e and f, which are genetically similar to serotype c, also had comparable polymorphism; however, serotypes a, b, d, g, and h did not hybridize to the same DNA probes in parallel experiments. Further analysis of enzymatic activities for glucan synthesis and sucrose-dependent adherence revealed no significant differences among the serotype c strains. Our results suggested that genetic polymorphisms existing in S. mutans serotype c strains may reflect a complexity in genes coding for the glucosyltransferases, which are produc

Release 3.1A John F. Collins, Biocomputing Research Unit.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jan 11 15:47:50 2000; MasPar time 2.45 Seconds
254.053 Million cell updates/sec

Tabulation output not generated.

Title: >US-09-290-049-3
Description: (1-22) from US09290049.pep
Perfect Score: 155
Sequence: 1 TGARTINGQLLYFRANGVQVKG 22

Scoring table: PAM 150
Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot37
1:swissprot

Statistics: Mean 29.681; Variance 38.978; scale 0.761

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	155	100.0	1475	1	GTFB_STRMU	GLUCOSYLTRANSFERASE-I	9.19e-23
2	114	73.5	1597	1	GTF1_STRDO	GLUCOSYLTRANSFERASE-I	4.74e-12
3	112	72.3	1592	1	GTF2_STRDO	GLUCOSYLTRANSFERASE-I	1.49e-11
4	106	68.4	1375	1	GTFC_STRMU	GLUCOSYLTRANSFERASE-SI	4.46e-10
5	104	67.1	1365	1	GTFS_STRDO	GLUCOSYLTRANSFERASE-S	1.36e-09
6	93	60.0	1430	1	GTFD_STRMU	GLUCOSYLTRANSFERASE-S	5.53e-07
7	79	51.0	382	1	YJO7_YEAST	HYPOTHETICAL 44.9 KD P	7.50e-04
8	72	46.5	126	1	DOC_BPP1	DEATH ON CURING PROTEI	2.20e-02
9	70	45.2	529	1	Y119_NPVOP	HYPOTHETICAL 59.0 KD P	5.58e-02
10	67	43.2	2710	1	TOXA_CLODI	TOXIN A.	2.19e-01
11	65	41.9	349	1	PTER_MOUSE	PHOSPHOTRIESTERASE REL	5.32e-01
12	65	41.9	1396	1	VLTF_BPT5	L-SHAPED TAIL FIBRE PR	5.32e-01
13	63	40.6	301	1	LECI_MOUSE	ASIALOGLYCOPROTEIN REC	1.27e+00
14	63	40.6	310	1	YC08_PYRHO	HYPOTHETICAL SUGAR KIN	1.27e+00
15	63	40.6	349	1	PTER_RAT	PHOSPHOTRIESTERASE REL	1.27e+00
16	63	40.6	396	1	DUT_VZVD	DEOXYURIDINE 5'-TRIPHO	1.27e+00
17	63	40.6	404	1	CAG5_CHICK	ALPHA-N-ACETYLGALACTOS	1.27e+00
18	63	40.6	475	1	AP54_YEAST	CLATHRIN COAT ASSEMBLY	1.27e+00
19	63	40.6	1082	1	RRPO_ROTPC	RNA-DIRECTED RNA POLYM	1.27e+00
20	62	40.0	464	1	VL2_HPV27	MINOR CAPSID PROTEIN L	1.95e+00
21	62	40.0	467	1	ISP6_SCHPO	SEXUAL DIFFERENTIATION	1.95e+00
22	62	40.0	524	1	VL2_HPV2A	MINOR CAPSID PROTEIN L	1.95e+00
23	61	39.4	336	1	VINT_BP186	INTEGRASE.	2.97e+00
24	61	39.4	402	1	YIN2_STRAM	HYPOTHETICAL 44.6 KD P	2.97e+00
25	61	39.4	433	1	MURC_PORGI	UDP-N-ACETYLMURAMATE--	2.97e+00
26	61	39.4	691	1	LCN3_LACLA	LACTICIN 481/LACTOCOCC	2.97e+00
27	60	38.7	472	1	CB1R_FELCA	CANNABINOID RECEPTOR 1	4.51e+00
28	60	38.7	472	1	CB1R_HUMAN	CANNABINOID RECEPTOR 1	4.51e+00
29	60	38.7	473	1	CB1R_RAT	CANNABINOID RECEPTOR 1	4.51e+00
30	60	38.7	473	1	CB1R_MOUSE	CANNABINOID RECEPTOR 1	4.51e+00
31	60	38.7	513	1	Y073_TREPA	HYPOTHETICAL PROTEIN T	4.51e+00
32	60	38.7	696	1	SP1_HUMAN	TRANSCRIPTION FACTOR S	4.51e+00
33	60	38.7	788	1	SP1_RAT	TRANSCRIPTION FACTOR S	4.51e+00
34	59	38.1	264	1	YED6_SCHPO	HYPOTHETICAL 30.7 KD P	6.81e+00
35	59	38.1	299	1	YQO2_CAEEL	HYPOTHETICAL 35.2 KD P	6.81e+00
36	59	38.1	527	1	Y096_MYCGE	HYPOTHETICAL PROTEIN M	6.81e+00
37	59	38.1	998	1	EPA7_RAT	EPHRIN TYPE-A RECEPTOR	6.81e+00
38	59	38.1	998	1	EPA7_HUMAN	EPHRIN TYPE-A RECEPTOR	6.81e+00
39	59	38.1	998	1	EPA7_MOUSE	EPHRIN TYPE-A RECEPTOR	6.81e+00
40	59	38.1	1581	1	ARO1_PNECA	PENTAFUNCTIONAL AROM P	6.81e+00
41	58	37.4	271	1	YDHO_ECOLI	HYPOTHETICAL 29.9 KD P	1.02e+01
42	58	37.4	806	1	ITB7_MOUSE	INTEGRIN BETA-7 SUBUNI	1.02e+01
43	58	37.4	931	1	PQQL_ECOLI	PROBABLE ZINC PROTEASE	1.02e+01
44	58	37.4	1064	1	KIN1_YEAST	PROTEIN KINASE KIN1 (E	1.02e+01
45	58	37.4	2067	1	BIMB_EMENI	CELL DIVISION-ASSOCIAT	1.02e+01

ALIGNMENTS

```
RESULT    1
ID   GTFB_STRMU     STANDARD;      PRT;  1475 AA.
AC   P08987;
DT   01-NOV-1988 (REL. 09, CREATED)
DT   01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
DT   15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE   GLUCOSYLTRANSFERASE-I PRECURSOR (EC 2.4.1.5) (GTF-I) (DEXTRANSUCRASE)
DE   (SUCROSE 6-GLUCOSYLTRANSFERASE).
GN   GTFB.
OS   STREPTOCOCCUS MUTANS.
OC   BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
OC   STREPTOCOCCUS.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GS-5;
RX   MEDLINE; 87308013.
RA   SHIROZA T., UEDA S., KURAMITSU H.K.;
RT   "Sequence analysis of the gtfB gene from Streptococcus mutans.";
RL   J. BACTERIOL. 169:4263-4270(1987).
CC   -!- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT
CC       TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE
CC       OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE
CC       AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.
CC   -!- CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL) (N) =
CC       D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL) (N+1).
CC   -!- SUBCELLULAR LOCATION: SECRETED.
CC   -!- DISEASE: DENTAL CARIES.
CC   -!- GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKED
CC       GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES WATER-SOLUBLE
CC       GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH FORMS OF
CC       GLUCANS.
CC   -!- SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES AND SOME TO A GLUCAN-
CC       BINDING PROTEIN FROM S.MUTANS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M17361; G153640; -.
DR   PIR; B33135; B33135.
DR   PFAM; PF00128; alpha-amylase; 1.
KW   TRANSFERASE; GLYCOSYLTRANSFERASE; SIGNAL; REPEAT; DENTAL CARIES.
FT   SIGNAL        1     34       POTENTIAL.
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FT   CHAIN        35   1475       GLUCOSYLTRANSFERASE-I.
FT   DOMAIN       35   1050       CATALYTIC (APPROXIMATE).
FT   DOMAIN     1096   1475       GLUCAN-BINDING (APPROXIMATE).
FT   REPEAT     1096   1129       A REPEAT.
FT   DOMAIN     1160   1469       5 X TANDEM REPEATS.
FT   REPEAT     1160   1209       1.
FT   REPEAT     1224   1274       2.
FT   REPEAT     1289   1339       3.
FT   REPEAT     1354   1404       4.
FT   REPEAT     1419   1469       5.
SQ   SEQUENCE   1475 AA;  165812 MW;  4542C1D6 CRC32;

  Query Match          100.0%;  Score 155;  DB 1;  Length 1475;
  Best Local Similarity 100.0%;  Pred. No. 9.19e-23;
  Matches    22;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    1300 TGARTINGQLLYFRANGVQVKG 1321
           ||||||||||||||||||||||
Qy       1 TGARTINGQLLYFRANGVQVKG 22


RESULT    2
ID   GTF1_STRDO     STANDARD;      PRT;  1597 AA.
AC   [redacted]1001;
DT   [redacted]-JUL-1989 (REL. 11, CREATED)
DT   01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
DT   15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE   GLUCOSYLTRANSFERASE-I PRECURSOR (EC 2.4.1.5) (GTF-I) (DEXTRANSUCRASE)
DE   (SUCROSE 6-GLUCOSYLTRANSFERASE).
GN   GTFI.
OS   STREPTOCOCCUS DOWNEI (STREPTOCOCCUS SOBRINUS).
OC   BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
OC   STREPTOCOCCUS.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MFE28;
RX   MEDLINE; 87308014.
RA   FERRETTI J.J., GILPIN M.L., RUSSELL R.R.B.;
RT   "Nucleotide sequence of a glucosyltransferase gene from Streptococcus
RT   sobrinus MFe28.";
RL   J. BACTERIOL. 169:4271-4278(1987).
CC   -!- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT
CC       TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE
CC       OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE
CC       AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.
CC   -!- CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N) =
CC       D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).
CC   -!- SUBCELLULAR LOCATION: SECRETED.
CC   -!- DISEASE: DENTAL CARIES.
CC   -!- GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKED
CC       GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES WATER-SOLUBLE
CC       [redacted]GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH FORMS OF
CC       GLUCANS.
CC   -!- SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES AND SOME TO A GLUCAN-
CC       BINDING PROTEIN FROM S.MUTANS.
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CC   ---------------------------------------------------------------------
DR   EMBL; M17391; G153647; -.
DR   PFAM; PF00128; alpha-amylase; 1.
KW   TRANSFERASE; GLYCOSYLTRANSFERASE; SIGNAL; REPEAT; DENTAL CARIES.
FT   SIGNAL        1     38       POTENTIAL.
FT   CHAIN        39   1597       GLUCOSYLTRANSFERASE-I.
FT   DOMAIN       39   1050       CATALYTIC (APPROXIMATE).
FT   DOMAIN     1099   1597       GLUCAN-BINDING (APPROXIMATE).
FT   DOMAIN     1099   1597       1.25 A, 2 B, AND 5 AC REPEATS.
FT   REPEAT     1099   1132       A REPEAT.
FT   REPEAT     1163   1213       AC REPEAT.
FT   REPEAT     1227   1277       AC REPEAT.
FT   REPEAT     1292   1342       AC REPEAT.
FT   REPEAT     1352   1399       B REPEAT.
FT   REPEAT     1406   1455       AC REPEAT.
FT   REPEAT     1465   1512       B REPEAT.
FT   REPEAT     1519   1568       AC REPEAT.
FT   REPEAT     1582   1597       A REPEAT (INCOMPLETE).
SQ   SEQUENCE   1597 AA;  177080 MW;  995233CA CRC32;

  Query Match          73.5%;  Score 114;  DB 1;  Length 1597;
  Best Local Similarity 77.3%;  Pred. No. 4.74e-12;
  Matches    17;  Conservative    3;  Mismatches   2;  Indels   0;  Gaps   0;

Db    1303 TGAQTIKGQKLYFKANGQQVKG 1324
           |||:||:|| |||:|||| ||||
Qy       1 TGARTINGQLLYFRANGVQVKG 22


RESULT    3
ID   GTF2_STRDO     STANDARD;      PRT;  1592 AA.
AC   P27470;
DT   01-AUG-1992 (REL. 23, CREATED)
DT   01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
DT   15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE   GLUCOSYLTRANSFERASE-I PRECURSOR (EC 2.4.1.5) (GTF-I) (DEXTRANSUCRASE)
DE   (SUCROSE 6-GLUCOSYLTRANSFERASE).
OS   STREPTOCOCCUS DOWNEI (STREPTOCOCCUS SOBRINUS).
OC   BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
OC   STREPTOCOCCUS.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=6715;
RX   MEDLINE; 91123227.
RA   ABO H., MATSUMURA T., KODAMA T., OHTA H., FUKUI K., KATO K.,
RA   KAGAWA H.;
RT   "Peptide sequences for sucrose splitting and glucan binding within
RT   Streptococcus sobrinus glucosyltransferase (water-insoluble glucan
RT   synthetase).";
RL   J. BACTERIOL. 173:989-996(1991).
CC   -!- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT
CC       TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE
CC       OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE
CC       AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.
CC   -!- CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N) =
CC       D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).
CC   -!- SUBCELLULAR LOCATION: SECRETED.
CC   -!- DISEASE: DENTAL CARIES.
CC   -!- GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKED
CC       GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES WATER-SOLUBLE
CC       GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH FORMS OF
CC       GLUCANS.
CC   -!- SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES AND SOME TO A GLUCAN-
CC       BINDING PROTEIN FROM S.MUTANS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D90213; G217033; -.
DR   PIR; A38175; A38175.
DR   PFAM; PF00128; alpha-amylase; 1.
DR   HSSP; P00695; 2HEE.
KW   TRANSFERASE; GLYCOSYLTRANSFERASE; SIGNAL; REPEAT; DENTAL CARIES.
FT   SIGNAL        1     38       POTENTIAL.
FT   CHAIN        39   1592       GLUCOSYLTRANSFERASE-I.
FT   DOMAIN       39   1044       CATALYTIC (APPROXIMATE).
FT   DOMAIN     1093   1592       GLUCAN-BINDING (APPROXIMATE).
FT   DOMAIN     1093   1592       6.5 X TANDEM REPEATS.
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